

Fig.1

5'		9		18		27		36		45		54						
	ATG	GAA	ATT	ATT	TCA	TCA	AAA	CTA	TTC	ATT	TTA	TTG	ACT	TTA	GCC	ACT	TCA	AGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Glu	Ile	Ile	Ser	Ser	Lys	Leu	Phe	Ile	Leu	Leu	Thr	Leu	Ala	Thr	Ser	Ser
		63		72		81		90		99		108						
	TTG	TTA	ACA	TCA	AAC	ATT	TTT	TGT	GCA	GAT	GAA	TTA	GTG	ATG	TCC	AAT	CTT	CAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Ala	Asp	Glu	Leu	Val	Met	Ser	Asn	Leu	His
		117		126		135		144		153		162						
	AGC	AAA	GAA	AAT	TAT	GAC	AAA	TAT	TCT	GAG	CCT	AGA	GGA	TAC	CCA	AAA	GGG	GAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Lys	Glu	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg	Gly	Tyr	Pro	Lys	Gly	Glu
		171		180		189		198		207		216						
	AGA	AGC	CTC	AAT	TTT	GAG	GAA	TTA	AAA	GAT	TGG	GGA	CCA	AAA	AAT	GTT	ATT	AAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp	Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys
		225		234		243		252		261		270						
	ATG	AGT	ACA	CCT	GCA	GTC	AAT	AAA	ATG	CCA	CAC	TCC	TTC	GCC	AAC	TTG	CCA	TTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys	Met	Pro	His	Ser	Phe	Ala	Asn	Leu	Pro	Leu
		279		288		297		306		315		324						
	AGA	TTT	GGG	AGG	AAC	GTT	CAA	GAA	GAA	AGA	AGT	GCT	GGA	GCA	ACA	GCC	AAC	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Phe	Gly	Arg	Asn	Val	Gln	Glu	Glu	Arg	Ser	Ala	Gly	Ala	Thr	Ala	Asn	Leu
		333		342		351		360		369		378						
	CCT	CTG	AGA	TCT	GGA	AGA	AAT	ATG	GAG	GTG	AGC	CTC	GTG	AGA	CGT	GTT	CCT	AAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Pro	Leu	Arg	Ser	Gly	Arg	Asn	Met	Glu	Val	Ser	Leu	Val	Arg	Arg	Val	Pro	Asn
		387		396		405		414		423		432						
	CTG	CCC	CAA	AGG	TTT	GGG	AGA	ACA	ACA	GCC	AAA	AGT	GTC	TGC	AGG	ATG	CTG	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Ala	Lys	Ser	Val	Cys	Arg	Met	Leu	
		441		450		459		468		477		486						
	AGT	GAT	TTG	TGT	CAA	GGA	TCC	ATG	CAT	TCA	CCA	TGT	GCC	AAT	GAC	TTA	TTT	TAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Asp	Leu	Cys	Gln	Gly	Ser	Met	His	Ser	Pro	Cys	Ala	Asn	Asp	Leu	Phe	Tyr
		495		504		513		522		531		540						
	TCC	ATG	ACC	TGC	CAG	CAC	CAA	GAA	ATC	CAG	AAT	CCC	GAT	CAA	AAA	CAG	TCA	AGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Met	Thr	Cys	Gln	His	Gln	Glu	Ile	Gln	Asn	Pro	Asp	Gln	Lys	Gln	Ser	Arg

TAA 3'

Fig.2

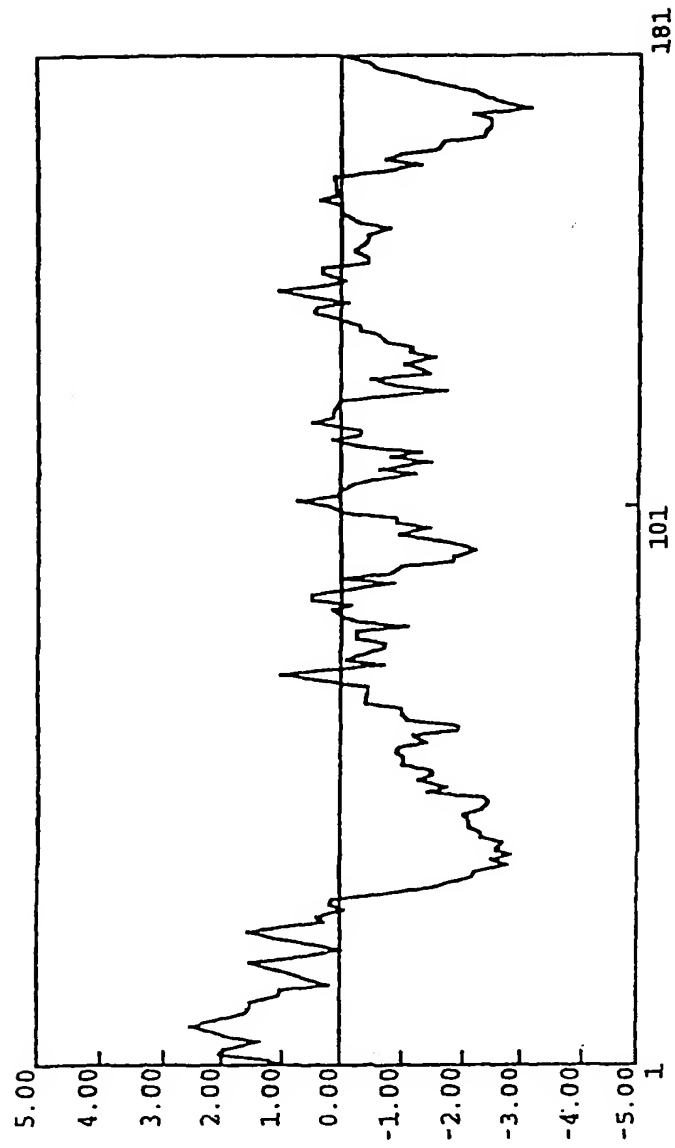


Fig.3

```

5'  ATG  GAA  ATT  ATT  TCA  TCA  AAA  CTA  TTC  ATT  TTA  TTG  ACT  TTA  GCC  ACT  TCA  AGC
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Met  Glu  Ile  Ile  Ser  Ser  Lys  Leu  Phe  Ile  Leu  Leu  Thr  Leu  Ala  Thr  Ser  Ser

      9      18      27      36      45      54
    TTG  TTA  ACA  TCA  AAC  ATT  TTT  TGT  GCA  GAT  GAA  TTA  GTG  ATG  TCC  AAT  CTT  CAC
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Leu  Leu  Thr  Ser  Asn  Ile  Phe  Cys  Ala  Asp  Glu  Leu  Val  Met  Ser  Asn  Leu  His

      63      72      81      90      99      108
    AGC  AAA  GAA  AAT  TAT  GAC  AAA  TAT  TCT  GAG  CCT  AGA  GGA  TAC  CCA  AAA  GGG  GAA
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Ser  Lys  Glu  Asn  Tyr  Asp  Lys  Tyr  Ser  Glu  Pro  Arg  Gly  Tyr  Pro  Lys  Gly  Glu

      117     126     135     144     153     162
    AGA  AGC  CTC  AAT  TTT  GAG  GAA  TTA  AAA  GAT  TGG  GGA  CCA  AAA  AAT  GTT  ATT  AAG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Arg  Ser  Leu  Asn  Phe  Glu  Glu  Leu  Lys  Asp  Trp  Gly  Pro  Lys  Asn  Val  Ile  Lys

      171     180     189     198     207     216
    ATG  AGT  ACA  CCT  GCA  GTC  AAT  AAA  ATG  CCA  CAC  TCC  TTC  GCC  AAC  TTG  CCA  TTG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Met  Ser  Thr  Pro  Ala  Val  Asn  Lys  Met  Pro  His  Ser  Phe  Ala  Asn  Leu  Pro  Leu

      225     234     243     252     261     270
    AGA  TTT  GGG  AGG  AAC  GTT  CAA  GAA  GAA  AGA  AGT  GCT  GGA  GCA  ACA  GCC  AAC  CTG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Arg  Phe  Gly  Arg  Asn  Val  Gln  Glu  Glu  Arg  Ser  Ala  Gly  Ala  Thr  Ala  Asn  Leu

      279     288     297     306     315     324
    CCT  CTG  AGA  TCT  GGA  AGA  AAT  ATG  GAG  GTG  AGC  CTC  GTG  AGA  CGT  GTT  CCT  AAC
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Pro  Leu  Arg  Ser  Gly  Arg  Asn  Met  Glu  Val  Ser  Leu  Val  Arg  Arg  Val  Pro  Asn

      333     342     351     360     369     378
    CTG  CCC  CAA  AGG  TTT  GGG  AGA  ACA  ACA  ACA  GCC  AAA  AGT  GTC  TGC  AGG  ATG  CTG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Leu  Pro  Gln  Arg  Phe  Gly  Arg  Thr  Thr  Thr  Ala  Lys  Ser  Val  Cys  Arg  Met  Leu

      387     396     405     414     423     432
    AGT  GAT  TTG  TGT  CAA  GGA  TCC  ATG  CAT  TCA  CCA  TGT  GCC  AAT  GAC  TTA  TTT  TAC
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Ser  Asp  Leu  Cys  Gln  Gly  Ser  Met  His  Ser  Pro  Cys  Ala  Asn  Asp  Leu  Phe  Tyr

      441     450     459     468     477     486
    TCC  ATG  ACC  TGC  CAG  CAC  CAA  GAA  ATC  CAG  AAT  CCC  GAT  CAA  AAA  CAG  TCA  AGG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Ser  Met  Thr  Cys  Gln  His  Gln  Glu  Ile  Gln  Asn  Pro  Asp  Gln  Lys  Gln  Ser  Arg

      495     504     513     522     531     540
    AGA  CTG  CTA  TTC  AAG  AAA  ATA  GAT  GAT  GCA  GAA  TTG  AAA  CAA  GAA  AAA  TAA  3'
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Arg  Leu  Leu  Phe  Lys  Lys  Ile  Asp  Asp  Ala  Glu  Leu  Lys  Gln  Glu  Lys  ***

```

Fig.4

		9		18		27		36		45		54						
5'	ATG	GAA	ATT	ATT	TCA	TTA	AAA	CGA	TTC	ATT	TTA	TTG	ATG	TTA	GCC	ACT	TCA	AGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Glu	Ile	Ile	Ser	Leu	Lys	Arg	Phe	Ile	Leu	Leu	Met	Leu	Ala	Thr	Ser	Ser
		63		72		81		90		99		108						
	TTG	TTA	ACA	TCA	AAC	ATC	TTC	TGC	ACA	GAC	GAA	TCA	AGG	ATG	CCC	AAT	CTT	TAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Thr	Asp	Glu	Ser	Arg	Met	Pro	Asn	Leu	Tyr
		117		126		135		144		153		162						
	AGC	AAA	AAG	AAT	TAT	GAC	AAA	TAT	TCC	GAG	CCT	AGA	GGA	GAT	CTA	GGC	TGG	GAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Lys	Lys	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg	Gly	Asp	Leu	Gly	Trp	Glu
		171		180		189		198		207		216						
	AAA	GAA	AGA	AGT	CTT	ACT	TTT	GAA	GAA	GTA	AAA	GAT	TGG	GCT	CCA	AAA	ATT	AAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Lys	Glu	Arg	Ser	Leu	Thr	Phe	Glu	Glu	Val	Lys	Asp	Trp	Ala	Pro	Lys	Ile	Lys
		225		234		243		252		261		270						
	ATG	AAT	AAA	CCT	GTA	GTC	AAC	AAA	ATG	CCA	CCT	TCT	GCA	GCC	AAC	CTG	CCA	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Asn	Lys	Pro	Val	Val	Asn	Lys	Met	Pro	Pro	Ser	Ala	Ala	Asn	Leu	Pro	Leu
		279		288		297		306		315		324						
	AGA	TTT	GGG	AGG	AAC	ATG	GAA	GAA	GAA	AGG	AGC	ACT	AGG	GCG	ATG	GCC	CAC	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Phe	Gly	Arg	Asn	Met	Glu	Glu	Glu	Arg	Ser	Thr	Arg	Ala	Met	Ala	His	Leu
		333		342		351		360		369		378						
	CCT	CTG	AGA	CTC	GGA	AAA	AAT	AGA	GAG	GAC	AGC	CTC	TCC	AGA	TGG	GTC	CCA	AAT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Pro	Leu	Arg	Leu	Gly	Lys	Asn	Arg	Glu	Asp	Ser	Leu	Ser	Arg	Trp	Val	Pro	Asn
		387		396		405		414		423		432						
	CTG	CCC	CAG	AGG	TTT	GGA	AGA	ACA	ACA	ACA	GCC	AAA	AGC	ATT	ACC	AAG	ACC	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Ile	Thr	Lys	Thr	Leu
		441		450		459		468		477		486						
	AGT	AAT	TTG	CTC	CAG	CAG	TCC	ATG	CAT	TCA	CCA	TCT	ACC	AAT	GGG	CTA	CTC	TAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Asn	Leu	Leu	Gln	Gln	Ser	Met	His	Ser	Pro	Ser	Thr	Asn	Gly	Leu	Leu	Tyr
		495		504		513		522		531		540						
	TCC	ATG	GCC	TGC	CAG	CCC	CAA	GAA	ATC	CAG	AAT	CCT	GGT	CAA	AAG	AAC	CTA	AGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Met	Ala	Cys	Gln	Pro	Gln	Glu	Ile	Gln	Asn	Pro	Gly	Gln	Lys	Asn	Leu	Arg
		549		558		567		576		585								
	AGA	CGG	GGA	TTC	CAG	AAA	ATA	GAT	GAT	GCA	GAA	TTG	AAA	CAA	GAA	AAA	TAA	3'
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Arg	Gly	Phe	Gln	Lys	Ile	Asp	Asp	Ala	Glu	Leu	Lys	Gln	Glu	Lys	***	

Fig.5

	9			18			27			36			45			54		
5'	ATG	GAA	ATT	ATT	TCA	TCA	AAG	CGA	TTC	ATT	TTA	TTG	ACT	TTA	GCA	ACT	TCA	AGC
	Met	Glu	Ile	Ile	Ser	Ser	Lys	Arg	Phe	Ile	Leu	Leu	Thr	Leu	Ala	Thr	Ser	Ser
	63			72			81			90			99			108		
	TTC	TTA	ACT	TCA	AAC	ACC	CTT	TGT	TCA	GAT	GAA	TTA	ATG	ATG	CCC	CAT	TTT	CAC
	Phe	Leu	Thr	Ser	Asn	Thr	Leu	Cys	Ser	Asp	Glu	Leu	Met	Met	Pro	His	Phe	His
	117			126			135			144			153			162		
	AGC	AAA	GAA	GGT	TAT	GGA	AAA	TAT	TAC	CAG	GTG	AGA	GGA	ATC	CCA	AAA	GGG	GTA
	Ser	Lys	Glu	Gly	Tyr	Gly	Lys	Tyr	Tyr	Gln	Leu	Arg	Gly	Ile	Pro	Lys	Gly	Val
	171			180			189			198			207			216		
	AAG	GAA	AGA	AGT	GTG	ACT	TTT	CAA	GAA	CTC	AAA	GAT	TGG	GGG	GCA	AAG	AAA	GAT
	Lys	Glu	Arg	Ser	Val	Thr	Phe	Gln	Glu	Leu	Lys	Asp	Trp	Gly	Ala	Lys	Lys	Asp
	225			234			243			252			261			270		
	ATT	AAG	ATG	AGT	CCA	GCC	CCT	GCC	AAC	AAA	GTG	CCC	CAC	TCA	GCA	GCC	AAC	CTT
	Ile	Lys	Met	Ser	Pro	Ala	Pro	Ala	Asn	Lys	Val	Pro	His	Ser	Ala	Ala	Asn	Leu
	279			288			297			306			315			324		
	CCC	CTG	AGG	TTT	GGG	AGG	AAC	ATA	GAA	GAC	AGA	AGA	AGC	CCC	AGG	GCA	CGG	GCC
	Pro	Leu	Arg	Phe	Gly	Arg	Asn	Ile	Glu	Asp	Arg	Arg	Ser	Pro	Arg	Ala	Arg	Ala
	333			342			351			360			369			378		
	AAC	ATG	GAG	GCA	GGG	ACC	ATG	AGC	CAT	TTT	CCC	AGC	CTG	CCC	CAA	AGG	TTT	GGG
	Asn	Met	Glu	Ala	Gly	Thr	Met	Ser	His	Phe	Pro	Ser	Leu	Pro	Gln	Arg	Phe	Gly
	387			396			405			414			423			432		
	AGA	ACA	ACA	GCC	AGA	CGC	ATC	ACC	AAG	ACA	CTG	GCT	GGT	TTG	CCC	CAG	AAA	TCC
	Arg	Thr	Thr	Ala	Arg	Arg	Ile	Thr	Lys	Thr	Leu	Ala	Gly	Leu	Pro	Gln	Lys	Ser
	441			450			459			468			477			486		
	CTG	CAC	TCC	CTG	GCC	TCC	AGT	GAA	TCG	CTC	TAT	GCC	ATG	ACC	CGC	CAG	CAT	CAA
	Leu	His	Ser	Leu	Ala	Ser	Ser	Glu	Ser	Leu	Tyr	Ala	Met	Thr	Arg	Gln	His	Gln
	495			504			513			522			531			540		
	GAA	ATT	CAG	AGT	CCT	GGT	CAA	GAC	CAA	CCT	AGG	AAA	CGC	GTG	TTC	ACG	GAA	ACA
	Glu	Ile	Gln	Ser	Pro	Gly	Gln	Glu	Gln	Pro	Arg	Lys	Arg	Val	Phe	Thr	Glu	Thr
	549			558			567			576			585			594		
	GAT	GAT	GCA	GAA	AGG	AAA	CAA	GAA	AAA	ATA	GGA	AAC	CTC	CAG	CCA	GTC	CTT	CAA
	Asp	Asp	Ala	Glu	Arg	Lys	Gln	Glu	Lys	Ile	Gly	Asn	Leu	Gln	Pro	Val	Leu	Gln
	603			612														
	GGG	GCT	ATG	AAG	CTG	TGA	3'											
	Gly	Ala	Met	Lys	Leu	***												

Fig.6

hLPLRF.aa	1	MEIIS	KRFI	LI	LT	AT	SS	LL	TS	NI	F	CA	DEL	V	S	N	L	H	S	K	E	N	Y	D	K	Y	S	E	P	R	G	50																					
bLPLRF.aa	1	MEIIS	KRFI	LI	LT	AT	SS	LL	TS	NI	F	CA	DES	R	M	P	N	L	H	S	K	E	N	Y	D	K	Y	S	E	P	R	G	50																				
rLPLRF.aa	1	MEIIS	KRFI	LI	LT	AT	SS	FL	TS	NI	F	CA	DEL	M	E	F	H	S	K	E	G	Y	K	Y	Q	I	R	G	I			50																					
hLPLRF.aa	51	--Y	P	K	G	---	E	R	S	L	F	E	E	L	K	D	W	G	P	K	N	V	I	K	M	S	T	E	A	N	L	P	L	R	F	G	R	N	100														
bLPLRF.aa	51	L	G	W	E	K	---	E	R	S	L	F	E	E	V	K	W	A	P	K	---	I	K	M	N	K	E	V	A	N	L	P	L	R	F	G	R	N	100														
rLPLRF.aa	51	---	P	K	G	V	K	E	R	S	L	F	E	E	L	K	D	W	G	A	K	I	L	K	M	S	P	A	P	A	N	L	P	L	R	F	G	R	N	100													
hLPLRF.aa	101	V	Q	E	R	S	A	G	A	T	A	N	L	P	L	R	S	G	R	N	M	E	V	S	L	F	E	E	V	K	W	P	N	L	P	Q	R	F	G	R	T	T	A	K	S	V	C	R	M	L	S	150	
bLPLRF.aa	101	M	E	E	R	S	I	F	R	A	M	A	N	L	P	L	R	S	G	R	N	R	E	I	S	L	F	E	E	V	K	W	P	N	L	P	Q	R	F	G	R	T	T	A	K	S	I	T	K	T	L	S	150
rLPLRF.aa	101	I	E	D	R	S	P	R	A	R	A	N	M	---	---	---	---	---	---	---	E	A	G	T	S	H	F	E	S	L	P	Q	R	F	G	R	T	T	A	R	R	I	T	K	T	L	A	150					
hLPLRF.aa	151	D	I	Q	S	M	H	S	E	C	A	N	L	F	E	S	M	T	C	Q	H	E	I	Q	N	E	D	Q	K	S	R	R	L	L	E	K	K	I	D	D	A	E	L	K	Q	E	200						
bLPLRF.aa	151	N	L	Q	S	M	H	S	E	S	I	N	G	L	L	Y	S	M	A	C	Q	H	E	I	Q	N	E	D	Q	K	N	L	R	R	R	F	Q	K	I	D	D	A	E	L	K	Q	E	200					
rLPLRF.aa	151	G	L	P	K	S	L	H	S	E	A	S	S	E	S	L	Y	A	M	I	R	O	H	E	I	Q	S	P	G	Q	E	P	R	R	V	E	T	E	I	D	D	A	E	R	K	Q	E	200					
hLPLRF.aa	201	K	*	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	250				
bLPLRF.aa	201	K	*	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	250					
rLPLRF.aa	201	K	I	G	N	L	Q	P	V	L	Q	G	A	M	K	L	*	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	250					

Fig.7

1	TTTAGACTTAGACGAAATGGAAATTATTTTCATTAAAACGATTCATTTTATTGACTGTG	58
1	MetGluIleIleSerLeuLysArgPheIleLeuLeuThrVal	14
59	GCAACTTCAAGCTTCTTAACATCAAACACCTTCTGTACAGATGAGTTCATGATGCCTCAT	118
15	AlaThrSerSerPheLeuThrSerAsnThrPheCysThrAspGluPheMetMetProHis	34
119	TTTCACAGCAAAGAAGGTGACGGAAAATACTCCCAGCTGAGAGGAATCCCAAAAGGGGAA	178
35	PheHisSerLysGluGlyAspGlyLysTyrSerGlnLeuArgGlyIleProLysGlyGlu	54
179	AAGGAAAGAAGTGTCAAGTTTTCAAGAACTAAAAGATTGGGGGGCAAAGAATGTTATTAAG	238
55	LysGluArgSerValSerPheGlnGluLeuLysAspTrpGlyAlaLysAsnValIleLys	74
239	ATGAGTCCAGCCCCTGCCAACAAAGTGCCCCACTCAGCAGCCAACCTGCCCTGAGATTT	298
75	MetSerProAlaProAlaAsnLysValProHisSerAlaAlaAsnLeuProLeuArgPhe	94
299	GGAAGGACCATAGATGAGAAAAGAAGCCCCGCAGCACGGGTCAACATGGAGGCAGGGACC	358
95	GlyArgThrIleAspGluLysArgSerProAlaAlaArgValAsnMetGluAlaGlyThr	114
359	AGGAGCCATTTCCCCAGCCTGCCCCAAAGGTTTGGGAGAACAACAGCCAGAAGCCCCAAG	418
115	ArgSerHisPheProSerLeuProGlnArgPheGlyArgThrThrAlaArgSerProLys	154
419	ACACCCGCTGATTTGCCACAGAAACCCCTGCACTCACTGGGCTCCAGCGAGTTGCTCTAC	538
135	ThrProAlaAspLeuProGlnLysProLeuHisSerLeuGlySerSerGluLeuLeuTyr	154
479	GTCATGATCTGCCAGCACCAAGAAATTCAGAGTCCTGGTGGAAAGCGAACGAGGAGAGGA	538
155	ValMetIleCysGlnHisGlnGluIleGlnSerProGlyGlyLysArgThrArgArgGly	174
539	GCGTTTGTGGAAACAGATGATGCAGAAAGGGAAACCAGAAAAATAGGAAACTCGAGCCCCG	598
175	AlaPheValGluThrAspAspAlaGluArgLysProGluLys***	188
599	ACTTCAAGAGGCTACGGAGC	618
188		188

Fig.8

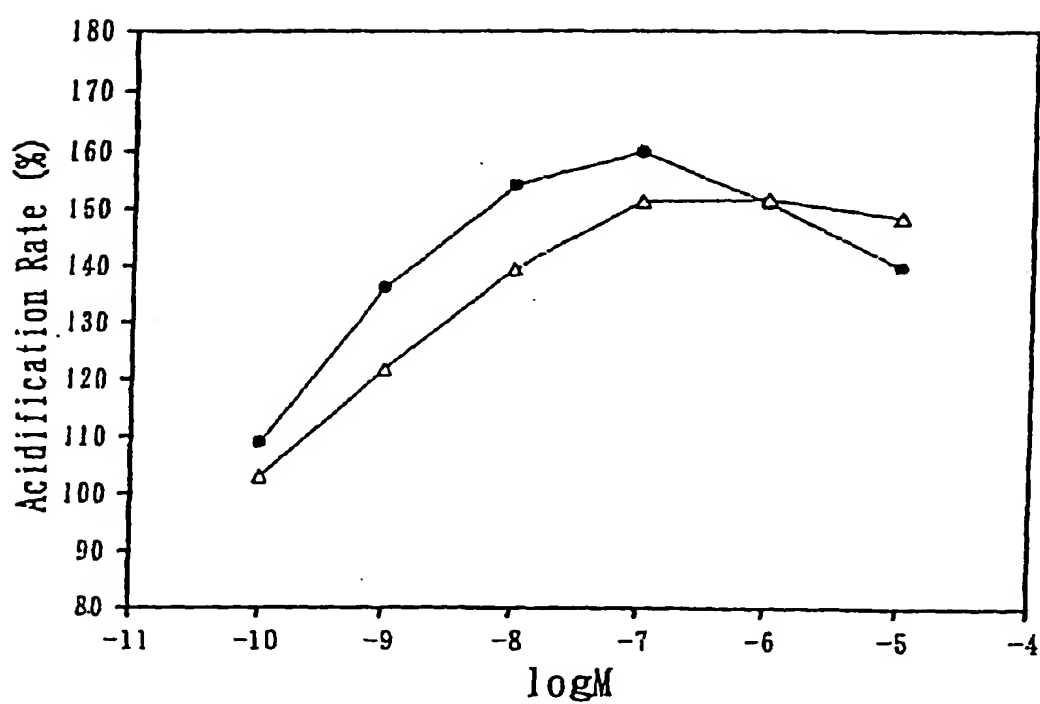


Fig.9

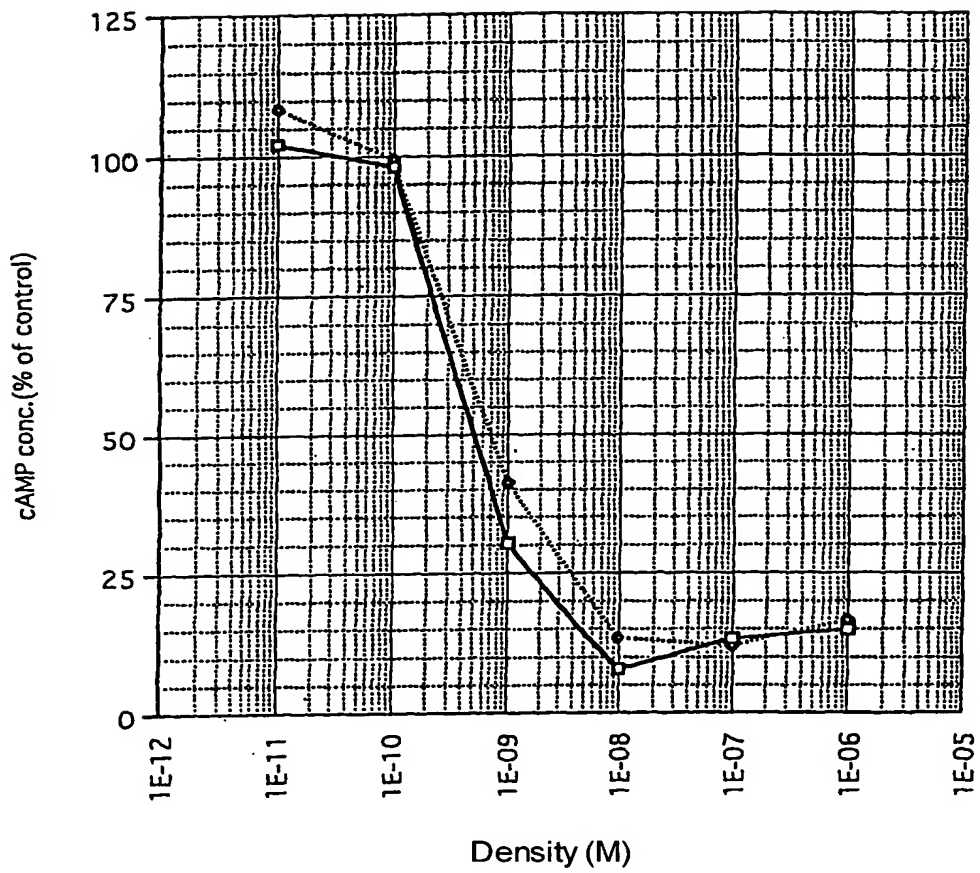


Fig.10

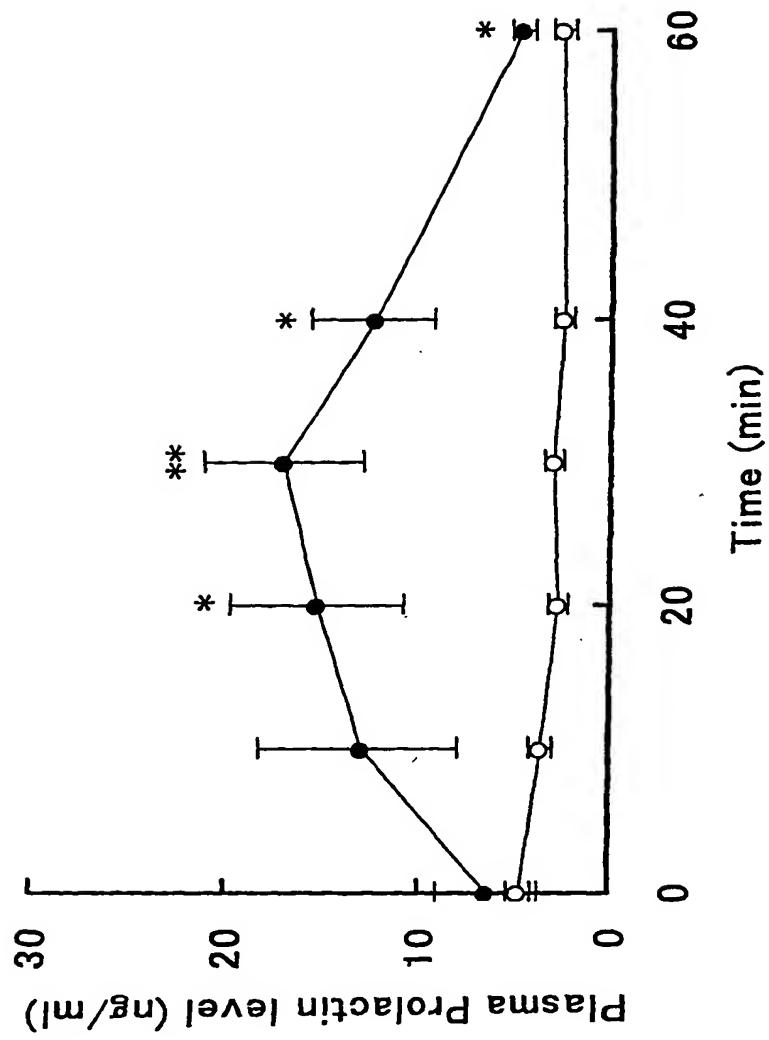
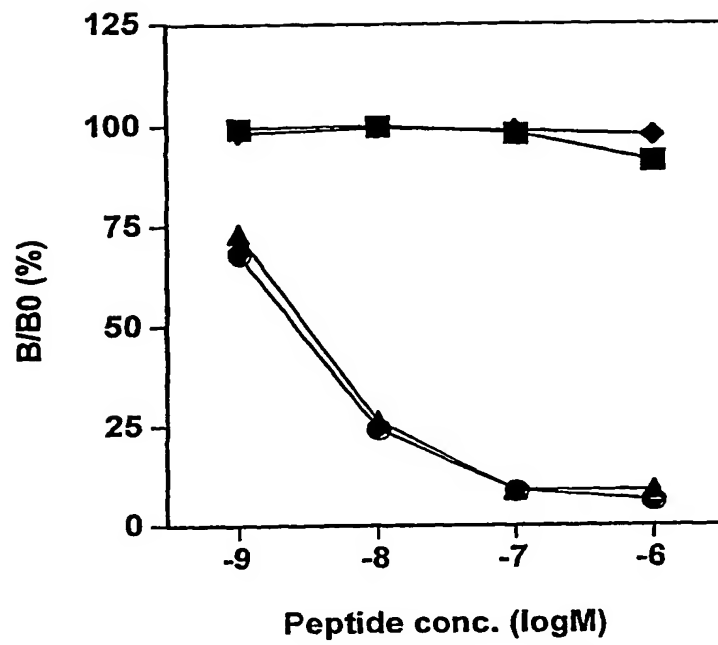


Fig.11



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Fig.12

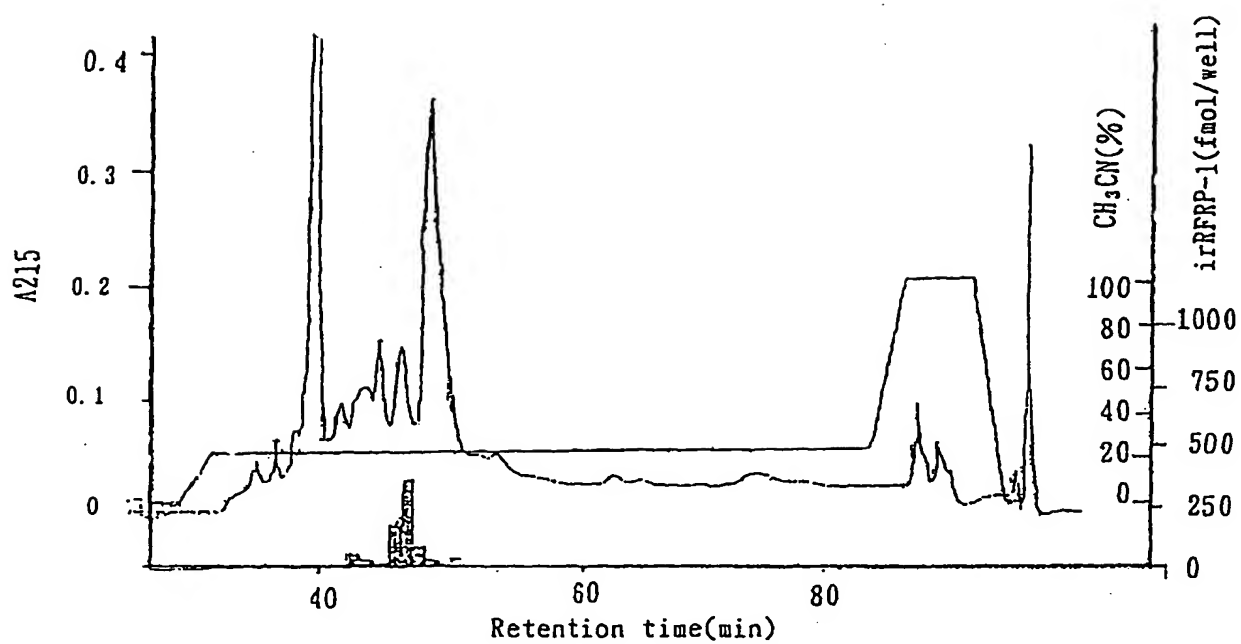


Fig.13

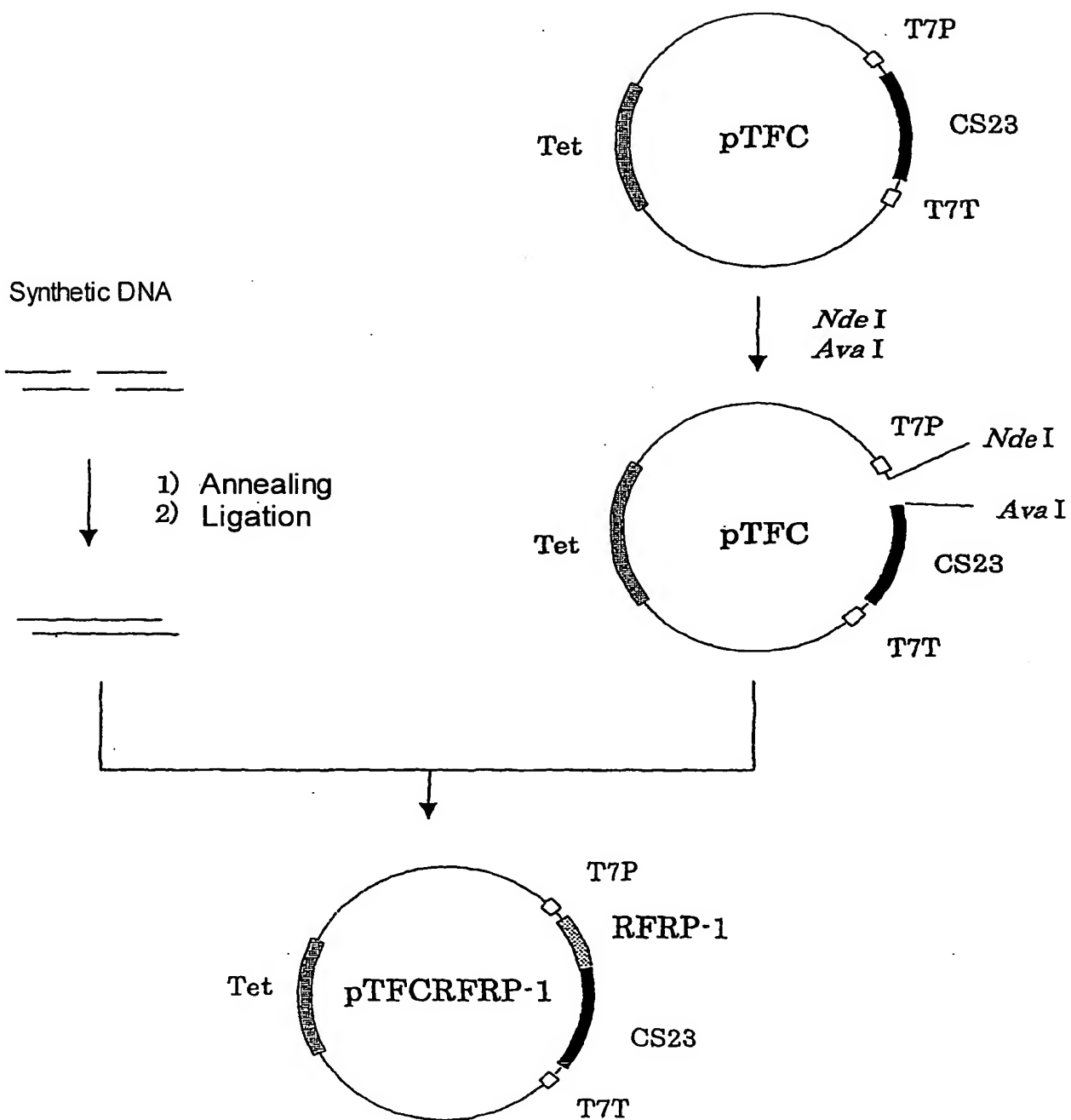


Fig.14

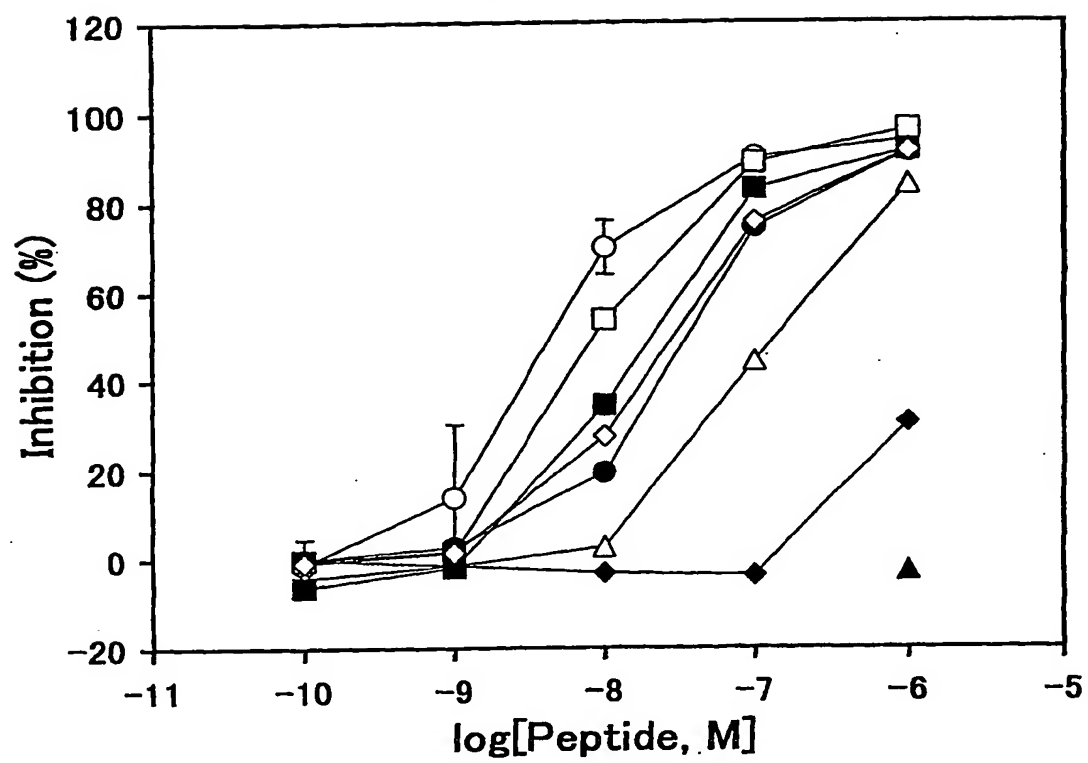


Fig.15

